



IFW16

RAW SEQUENCE LISTING

DATE: 07/26/2006

PATENT APPLICATION: US/10/632,780A

TIME: 09:34:00

Input Set : N:\Crf4\07252006\J632780.raw

Output Set: N:\CRF4\07252006\J632780A.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Philipp, Mario T.

3 (ii) TITLE OF INVENTION: Surface Antigens and Proteins Useful in
4 Compositions for the Diagnosis and Prevention of Lyme
5 Disease

6 (iii) NUMBER OF SEQUENCES: 14

7 (iv) CORRESPONDENCE ADDRESS:

8 (A) ADDRESSEE: Howson and Howson

9 (B) STREET: 501 Office Center Drive, Suite 210

10 (C) CITY: Fort Washington

11 (D) STATE: Pennsylvania

12 (E) COUNTRY: USA

13 (F) ZIP: 19034

14 (v) COMPUTER READABLE FORM:

15 (A) MEDIUM TYPE: Floppy disk

16 (B) COMPUTER: IBM PC compatible

17 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

18 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

19 (vi) CURRENT APPLICATION DATA:

C--> 20 (A) APPLICATION NUMBER: US/10/632,780A

C--> 21 (B) FILING DATE: 01-Aug-2003

22 (C) CLASSIFICATION:

23 (vii) PRIOR APPLICATION DATA:

W--> 24 (A) APPLICATION NUMBER: US 09/445,803

25 (B) FILING DATE: 13-DEC-1999

W--> 26 (A) APPLICATION NUMBER: PCT/US98/13551

27 (B) FILING DATE: 29-JUN-1998

W--> 28 (A) APPLICATION NUMBER: US 60/051,271

29 (B) FILING DATE: 30-JUN-1997

30 (viii) ATTORNEY/AGENT INFORMATION:

31 (A) NAME: Bak, Mary E.

32 (B) REGISTRATION NUMBER: 31,215

33 (C) REFERENCE/DOCKET NUMBER: TUL2BUSA

34 (ix) TELECOMMUNICATION INFORMATION:

35 (A) TELEPHONE: 215-540-9200

36 (B) TELEFAX: 215-540-5818

37 (2) INFORMATION FOR SEQ ID NO: 1:

38 (i) SEQUENCE CHARACTERISTICS:

39 (A) LENGTH: 1047 base pairs

40 (B) TYPE: nucleic acid

41 (C) STRANDEDNESS: double

42 (D) TOPOLOGY: unknown

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43 (ii) MOLECULE TYPE: cDNA
44 (ix) FEATURE:
45 (A) NAME/KEY: CDS
46 (B) LOCATION: 1..1047
47 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
48 AAG AAT AAT GAT CAT GAT AAT CAT AAG GGG ACT GTT AAG AAT GCT GTT 48
49 Lys Asn Asn Asp His Asp Asn His Lys Gly Thr Val Lys Asn Ala Val
50 1 5 10 15
51 GAT ATG GCA AAG GCC GCT GAG GAA GCT GCA AGT GCT GCA AGT GCT GCT 96
52 Asp Met Ala Lys Ala Ala Glu Glu Ala Ser Ala Ala Ser Ala Ala
53 20 25 30
54 ACT GGT AAT GCA GCG ATT GGG GAT GTT GTT AAG AAT AGT GGG GCA GCA 144
55 Thr Gly Asn Ala Ala Ile Gly Asp Val Val Lys Asn Ser Gly Ala Ala
56 35 40 45
57 GCA AAA GGT GGT GAG GCG GCG AGT GTT AAT GGG ATT GCT AAG GGG ATA 192
58 Ala Lys Gly Gly Glu Ala Ala Ser Val Asn Gly Ile Ala Lys Gly Ile
59 50 55 60
60 AAG GGG ATT GTT GAT GCT GCT GGA AAG GCT GAT GCG AAG GAA GGG AAG 240
61 Lys Gly Ile Val Asp Ala Ala Gly Lys Ala Asp Ala Lys Glu Gly Lys
62 65 70 75 80
63 TTG GAT GCT ACT GGT GCT GAG GGT ACG ACT AAC GTG AAT GCT GGG AAG 288
64 Leu Asp Ala Thr Gly Ala Glu Gly Thr Thr Asn Val Asn Ala Gly Lys
65 85 90 95
66 TTG TTT GTG AAG AGG GCG GCT GAT GAT GGT GGT GAT GCA GAT GAT GCT 336
67 Leu Phe Val Lys Arg Ala Ala Asp Asp Gly Gly Asp Ala Asp Ala
68 100 105 110
69 GGG AAG GCT GCT GCT GCG GTT GCT GCA AGT GCT GCT ACT GGT AAT GCA 384
70 Gly Lys Ala Ala Ala Val Ala Ala Ser Ala Ala Thr Gly Asn Ala
71 115 120 125
72 GCG ATT GGA GAT GTT GTT AAT GGT GAT GTG GCA AAA GCA AAA GGT GGT 432
73 Ala Ile Gly Asp Val Val Asn Gly Asp Val Ala Lys Ala Lys Gly Gly
74 130 135 140
75 GAT GCG GCG AGT GTT AAT GGG ATT GCT AAG GGT ATA AAG GGG ATT GTT 480
76 Asp Ala Ala Ser Val Asn Gly Ile Ala Lys Gly Ile Lys Gly Ile Val
77 145 150 155 160
78 GAT GCT GCT GAG AAG GCT GAT GCG AAG GAA GGG AAG TTG AAT GCT GCT 528
79 Asp Ala Ala Glu Lys Ala Asp Ala Lys Glu Gly Lys Leu Asn Ala Ala
80 165 170 175
81 GGT GCT GAG GGT ACG ACT AAC GCG GAT GCT GGG AAG TTG TTT GTG AAG 576
82 Gly Ala Glu Gly Thr Thr Asn Ala Asp Ala Gly Lys Leu Phe Val Lys
83 180 185 190
84 AAT GCT GGT AAT GTG GGT GGT GAA GCA GGT GAT GCT GGG AAG GCT GCT 624
85 Asn Ala Gly Asn Val Gly Gly Glu Ala Gly Asp Ala Gly Lys Ala Ala
86 195 200 205
87 GCT GCG GTT GCT GCT GTT AGT GGG GAG CAG ATA TTA AAA GCG ATT GTT 672
88 Ala Ala Val Ala Ala Val Ser Gly Glu Gln Ile Leu Lys Ala Ile Val
89 210 215 220
90 CAT GCT GCT AAG GAT GGT GGT GAG AAG CAG GGT AAG AAG GCT GCG GAT 720
91 His Ala Ala Lys Asp Gly Gly Glu Lys Gln Gly Lys Lys Ala Ala Asp

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92      225      230      235      240
93      CGT ACA AAT CCC ATT GAC GCG GCT ATT GGG GGT GCG GGT GAT AAT GAT      768
94      Arg Thr Asn Pro Ile Asp Ala Ala Ile Gly Gly Ala Gly Asp Asn Asp
95      245      250      255
96      GCT GCT GCG GCG TTT GCT ACT ATG AAG AAG GAT GAT CAG ATT GCT GCT      816
97      Ala Ala Ala Ala Phe Ala Thr Met Lys Lys Asp Asp Gln Ile Ala Ala
98      260      265      270
99      GCT ATG GTT CTG AGG GGA ATG GCT AAG GAT GGG CAA TTT GCT TTG AAG      864
100     Ala Met Val Leu Arg Gly Met Ala Lys Asp Gly Gln Phe Ala Leu Lys
101     275      280      285
102     GAT GCT GCT GCT GCT CAT GAA GGG ACT GTT AAG AAT GCT GTT GAT ATA      912
103     Asp Ala Ala Ala Ala His Glu Gly Thr Val Lys Asn Ala Val Asp Ile
104     290      295      300
105     ATA AAG GCT GCT GCG GAA GCT GCA AGT GCT GCA AGT GCT GCT ACT GGT      960
106     Ile Lys Ala Ala Ala Glu Ala Ala Ser Ala Ala Ser Ala Ala Thr Gly
107     305      310      315      320
108     AGT GCA GCA ATT GGG GAT GTT GTT AAT GGT AAT GGA GCA ACA GCA AAA      1008
109     Ser Ala Ala Ile Gly Asp Val Val Asn Gly Asn Gly Ala Thr Ala Lys
110     325      330      335
111     GGT GGT GAT GCG AAG AGT GTT AAT GGC ATT GCT AAG GGA      1047
112     Gly Gly Asp Ala Lys Ser Val Asn Gly Ile Ala Lys Gly
113     340      345

115 (2) INFORMATION FOR SEQ ID NO: 2:
116     (i) SEQUENCE CHARACTERISTICS:
117         (A) LENGTH: 349 amino acids
118         (B) TYPE: amino acid
119         (D) TOPOLOGY: linear
120     (ii) MOLECULE TYPE: protein
121     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
122     Lys Asn Asn Asp His Asp Asn His Lys Gly Thr Val Lys Asn Ala Val
123     1      5      10      15
124     Asp Met Ala Lys Ala Ala Glu Glu Ala Ala Ser Ala Ala Ser Ala Ala
125     20      25      30
126     Thr Gly Asn Ala Ala Ile Gly Asp Val Val Lys Asn Ser Gly Ala Ala
127     35      40      45
128     Ala Lys Gly Gly Glu Ala Ala Ser Val Asn Gly Ile Ala Lys Gly Ile
129     50      55      60
130     Lys Gly Ile Val Asp Ala Ala Gly Lys Ala Asp Ala Lys Glu Gly Lys
131     65      70      75      80
132     Leu Asp Ala Thr Gly Ala Glu Gly Thr Thr Asn Val Asn Ala Gly Lys
133     85      90      95
134     Leu Phe Val Lys Arg Ala Ala Asp Asp Gly Gly Asp Ala Asp Asp Ala
135     100     105     110
136     Gly Lys Ala Ala Ala Val Ala Ala Ser Ala Ala Thr Gly Asn Ala
137     115     120     125
138     Ala Ile Gly Asp Val Val Asn Gly Asp Val Ala Lys Ala Lys Gly Gly
139     130     135     140
140     Asp Ala Ala Ser Val Asn Gly Ile Ala Lys Gly Ile Lys Gly Ile Val
141     145     150     155     160

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142   Asp Ala Ala Glu Lys Ala Asp Ala Lys Glu Gly Lys Leu Asn Ala Ala
143               165                      170                      175
144   Gly Ala Glu Gly Thr Thr Asn Ala Asp Ala Gly Lys Leu Phe Val Lys
145               180                      185                      190
146   Asn Ala Gly Asn Val Gly Gly Glu Ala Gly Asp Ala Gly Lys Ala Ala
147               195                      200                      205
148   Ala Ala Val Ala Ala Val Ser Gly Glu Gln Ile Leu Lys Ala Ile Val
149               210                      215                      220
150   His Ala Ala Lys Asp Gly Gly Glu Lys Gln Gly Lys Lys Ala Ala Asp
151               225                      230                      235                      240
152   Arg Thr Asn Pro Ile Asp Ala Ala Ile Gly Gly Ala Gly Asp Asn Asp
153               245                      250                      255
154   Ala Ala Ala Ala Phe Ala Thr Met Lys Lys Asp Asp Gln Ile Ala Ala
155               260                      265                      270
156   Ala Met Val Leu Arg Gly Met Ala Lys Asp Gly Gln Phe Ala Leu Lys
157               275                      280                      285
158   Asp Ala Ala Ala Ala His Glu Gly Thr Val Lys Asn Ala Val Asp Ile
159               290                      295                      300
160   Ile Lys Ala Ala Ala Glu Ala Ala Ser Ala Ala Ser Ala Ala Thr Gly
161               305                      310                      315                      320
162   Ser Ala Ala Ile Gly Asp Val Val Asn Gly Asn Gly Ala Thr Ala Lys
163               325                      330                      335
164   Gly Gly Asp Ala Lys Ser Val Asn Gly Ile Ala Lys Gly
165               340                      345

167 (2) INFORMATION FOR SEQ ID NO: 3:
168     (i) SEQUENCE CHARACTERISTICS:
169         (A) LENGTH: 283 base pairs
170         (B) TYPE: nucleic acid
171         (C) STRANDEDNESS: double
172         (D) TOPOLOGY: unknown
173     (ii) MOLECULE TYPE: DNA (genomic)
174     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
175     GCCGCTGGAT GGTGGTGAGA AGCAGGGTAA GAAGGCTGCG GATCGTACAA ATCCCATTTGA      60
176     CGCGGCTATT GGGGGTGCGG GTGATAATGA TGCTGCTGCG GCGTTTGCTA CTATGAAGAA      120
177     GGATGATCAG ATTGCTGCTG CTATGGTTCT GAGGGGAATG GCTAAGGATG GGCAATTTGC      180
178     TTTGAAGGAT GCTGCTGCTG CTCATGAAGG GACTGTTAAG AATGCTGTTG ATATAATAAA      240
179     GGCTGCTGCG GAAGCTGCAA GTGCTGCAAG TGCTGCTACT GGT                          283

181 (2) INFORMATION FOR SEQ ID NO: 4:
182     (i) SEQUENCE CHARACTERISTICS:
183         (A) LENGTH: 233 base pairs
184         (B) TYPE: nucleic acid
185         (C) STRANDEDNESS: double
186         (D) TOPOLOGY: unknown
187     (ii) MOLECULE TYPE: DNA (genomic)
188     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
189     TTTATTATAT CAACAGATTC TTAACAGTCC CTTTCATGAGC AGCAGCAGCA TCCTTCAAAG      60
190     CAAATTGCCC ATCCTTAGCC ATTCCCTCA GAACCATAGC AGCAGCAATC TGATCATCCT      120
191     TCTTCATAGT AGCAAACGCC GCAGCAGCAT CATTATCACC CGCACCCTCA ATAGCCGCGT      180
192     CAATCGGATT TGTACGATCC GCAGCCTTCT TACCCTGCTT CTCACCACCA TCC              233

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194 (2) INFORMATION FOR SEQ ID NO: 5:

195 (i) SEQUENCE CHARACTERISTICS:

196 (A) LENGTH: 194 base pairs

197 (B) TYPE: nucleic acid

198 (C) STRANDEDNESS: double

199 (D) TOPOLOGY: unknown

200 (ii) MOLECULE TYPE: DNA (genomic)

201 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

202	CCGTGCAAGC TGGGTTGAAG AAGGTTGGGG ATGTTGTTAA GAATAGTGAG GCAAAAGATG	60
203	GTGATGCGGC GAGTGTTAAT GGGATTGCTA AGGGGATAAA GGGGATTGTT GATGCTGCTG	120
204	AGAAGGCTGA TGCGAAGGAA GGGAAGTTGG TATGTGGCTG GTGCTGCTGG TGAAACTAAC	180
205	AAGGAAGCGG CCGC	194

207 (2) INFORMATION FOR SEQ ID NO: 6:

208 (i) SEQUENCE CHARACTERISTICS:

209 (A) LENGTH: 369 base pairs

210 (B) TYPE: nucleic acid

211 (C) STRANDEDNESS: double

212 (D) TOPOLOGY: unknown

213 (ii) MOLECULE TYPE: DNA (genomic)

214 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

215	GCGGCCGCTT GAGGAAGCTG CAAGTGCTGC AAGTGCTGCT ACTGGTAATG CAGCGATTGG	60
216	GGATGTTGTT AAGAATAGTG GGGCAGCAGC AAAAGGTGGT GAGGCGGCCGA GTGTTAATGG	120
217	GATTGCTAAG GGGATAAAGG GGATTGTTGA TGCTGCTGGA AAGGCTGATG CGAAGGAAGG	180
218	GAAGTTGGAT GCTACTGGTG CTGAGGGTAC GACTAACGTG AATGCTGGGA AGTTGTTTGT	240
219	GAAGAGGGCG GCTGATGATG GTGGTGATGC AGATGATGCT GGGAAGGCTG CTGCTGCGGT	300
220	TGCTGCAAGT GCTGCTACTG GTAATGCAGC GATTGGAGAT GTTGTTAATG GTGATGTGGC	360
221	AAAACAAAA	369

223 (2) INFORMATION FOR SEQ ID NO: 7:

224 (i) SEQUENCE CHARACTERISTICS:

225 (A) LENGTH: 142 base pairs

226 (B) TYPE: nucleic acid

227 (C) STRANDEDNESS: double

228 (D) TOPOLOGY: unknown

229 (ii) MOLECULE TYPE: DNA (genomic)

230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

231	AAGGATGGTG ATGATAAGCA GGGTAAGAAG GCTGAGGATG CTACAAATCC GATTGACGCG	60
232	GCTATTGGGG GTGCAGGTGC GGGTGCTAAT GCTGCTGCGG CGTTTAATAA TATGAAGAAG	120
233	GATGATCAGA TTGAGCGGCC GC	142

235 (2) INFORMATION FOR SEQ ID NO: 8:

236 (i) SEQUENCE CHARACTERISTICS:

237 (A) LENGTH: 210 base pairs

238 (B) TYPE: nucleic acid

239 (C) STRANDEDNESS: double

240 (D) TOPOLOGY: unknown

241 (ii) MOLECULE TYPE: DNA (genomic)

242 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

243	GGTGAAACTA ACAAGGATGC TGGGAAGTTG TTTGTGAAGA AGAATGGTGA TGATGGTGGT	60
244	GATGCAGGTG ATGCTGGGAA GGCTGCTGCT GCGGTTGCTG CTGTTAGTGG GGAGCAGATA	120
245	TTAAAAGCGA TTGTTGATGC TGCTAAAGAT GGTGATAAGA CGGGGGTTAC TGATGTAAAG	180

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/26/2006
PATENT APPLICATION: US/10/632,780A TIME: 09:34:01

Input Set : N:\Crf4\07252006\J632780.raw
Output Set: N:\CRF4\07252006\J632780A.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

VERIFICATION SUMMARY

DATE: 07/26/2006

PATENT APPLICATION: US/10/632,780A

TIME: 09:34:01

Input Set : N:\Crf4\07252006\J632780.raw

Output Set: N:\CRF4\07252006\J632780A.raw

L:20 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:21 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:26 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)
L:28 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)